

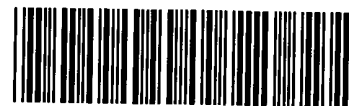
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MAR 08 2002

Page 1 of 7

#11

TECH CENTER 1600/2900



REC

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ENTERED

1636

RAW SEQUENCE

PATENT APPLICATION: US/09/659,737A

DATE: 02/26/2002

TIME: 13:59:19

Input Set : A:\71369-172(PFI-024US).ST25.txt

Output Set: N:\CRF3\02262002\I659737A.raw

3 <110> APPLICANT: Blumenberg, Miroslav
4 Gazel, Alix M.
6 <120> TITLE OF INVENTION: Genes and Polynucleotides Associated with Ultraviolet
7 Radiation-Mediated Skin Damage and Uses Thereof
9 <130> FILE REFERENCE: 71369.172(PFI-024US)
11 <140> CURRENT APPLICATION NUMBER: US 09/659,737A
12 <141> CURRENT FILING DATE: 2000-09-11
14 <150> PRIOR APPLICATION NUMBER: US 60/155,029
15 <151> PRIOR FILING DATE: 1999-09-20
17 <160> NUMBER OF SEQ ID NOS: 19
19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 164
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (2)...(163)
30 <400> SEQUENCE: 1
31 g cac cgg gac atc aag gca gga aat att ttg cta ctt gag aag ata gaa 49
32 His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Leu Glu Lys Ile Glu
33 1 5 10 15
35 cat gat gac atc tgc aat aaa act ttg aag att aca gat ttt ggg ttg 97
36 His Asp Asp Ile Cys Asn Lys Thr Leu Lys Ile Thr Asp Phe Gly Leu
37 20 25 30
39 gcg agg gaa tgg cac agg acc acc aaa atg agc aca gca ggc acc tat 145
40 Ala Arg Glu Trp His Arg Thr Thr Lys Met Ser Thr Ala Gly Thr Tyr
41 35 40 45
43 gcc tgg atg gcc cca gaa g 164
44 Ala Trp Met Ala Pro Glu
45 50
48 <210> SEQ ID NO: 2
49 <211> LENGTH: 54
50 <212> TYPE: PRT
51 <213> ORGANISM: Homo sapiens
53 <400> SEQUENCE: 2
54 His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Leu Glu Lys Ile Glu
55 1 5 10 15
56 His Asp Asp Ile Cys Asn Lys Thr Leu Lys Ile Thr Asp Phe Gly Leu
57 20 25 30
58 Ala Arg Glu Trp His Arg Thr Thr Lys Met Ser Thr Ala Gly Thr Tyr
59 35 40 45
60 Ala Trp Met Ala Pro Glu

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Input Set : A:\71369-172(PFI-024US).ST25.txt

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61      50
64 <210> SEQ ID NO: 3
65 <211> LENGTH: 145
66 <212> TYPE: DNA
67 <213> ORGANISM: Homo sapiens
69 <220> FEATURE:
70 <221> NAME/KEY: CDS
71 <222> LOCATION: (2)...(145)
73 <400> SEQUENCE: 3
74 a cat cgg gac atc aag agc gac tcg atc ctg ctg acc cat gat ggc agg 49
75   His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr His Asp Gly Arg
76     1           5           10           15
78 gtg aag ctg tca gac ttt ggg ttc tgc gcc cag gtg agc aag gaa gtg 97
79 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Val Ser Lys Glu Val
80           20           25           30
82 ccc cga agg aag tcg ctg gtc ggc acg ccc tac tgg atg gcc cca gag 145
83 Pro Arg Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
84     35           40           45
88 <210> SEQ ID NO: 4
89 <211> LENGTH: 48
90 <212> TYPE: PRT
91 <213> ORGANISM: Homo sapiens
93 <400> SEQUENCE: 4
94 His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr His Asp Gly Arg
95     1           5           10           15
96 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Val Ser Lys Glu Val
97           20           25           30
98 Pro Arg Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
99     35           40           45
102 <210> SEQ ID NO: 5
103 <211> LENGTH: 146
104 <212> TYPE: DNA
105 <213> ORGANISM: Homo sapiens
107 <220> FEATURE:
108 <221> NAME/KEY: CDS
109 <222> LOCATION: (2)...(145)
111 <400> SEQUENCE: 5
112 t cac agg gac atc aag agt gac tcc atc ctg ctg acc ctc gat ggc agg 49
113   His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr Leu Asp Gly Arg
114     1           5           10           15
116 gtg aag ctc tcg gac ttc gga ttc tgt gct cag atc agc aaa gac gtc 97
117 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Ile Ser Lys Asp Val
118           20           25           30
120 cct aag agg aag tcc ctg gtg gga acc ccc tac tgg atg gcg ccc gag 145
121 Pro Lys Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
122     35           40           45
124 g
126 <210> SEQ ID NO: 6
127 <211> LENGTH: 48

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RAW SEQUENCE LISTING

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Output Set: N:\CRF3\02262002\I659737A.raw

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128 <212> TYPE: PRT
129 <213> ORGANISM: Homo sapiens
131 <400> SEQUENCE: 6
132 His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr Leu Asp Gly Arg
133 1 5 10 15
134 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Ile Ser Lys Asp Val
135 20 25 30
136 Pro Lys Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
137 35 40 45
140 <210> SEQ ID NO: 7
141 <211> LENGTH: 3627
142 <212> TYPE: DNA
143 <213> ORGANISM: Homo sapiens
145 <220> FEATURE:
146 <221> NAME/KEY: CDS
147 <222> LOCATION: (868)..(1275)
149 <220> FEATURE:
150 <221> NAME/KEY: CDS
151 <222> LOCATION: (1420)..(1553)
153 <220> FEATURE:
154 <221> NAME/KEY: CDS
155 <222> LOCATION: (1900)..(2026)
157 <220> FEATURE:
158 <221> NAME/KEY: CDS
159 <222> LOCATION: (2105)..(2230)
161 <220> FEATURE:
162 <221> NAME/KEY: CDS
163 <222> LOCATION: (2696)..(2833)
165 <400> SEQUENCE: 7
166 gatctgcgac ctccttcaga acctgccaaa atgactagga aaaatgctgt ttccatagca 60
167 agagccaaaa gagaacatga cggccctgca ctccgggata tctctggcac cagattccca 120
168 gcccgaggga gacacctgaa cccccagat ggtgacacac ctctgtggtc ctctgtcagg 180
169 gacataacct ccagcacag atttgcaaac tccctgctgc aggcacaagc agggctatcg 240
170 ggccccaggt gtggtcctcc tgccttggtt cagggagtgg agacacagtt gccactgct 300
171 cccaccccca ctgccaggcc tcttctgccc ccattgggtc tggggtgggg gagccttggg 360
172 agttgaagaa tgcctctgac ccagattctt caagcagcct ctgagctcag aggaagagtc 420
173 tgcctcacgg cagcctccct ggggtctagc tgtcaatcgc ccaggaagaa ataccagcg 480
174 cgggaccggg cggggaagct ggccttctct gtcttcccag gtgcagcaca gcgagtgtaa 540
175 ggagctgtct tgggcctgcc cagcctggtg ccctgcgggg gactgctggc acaggactgt 600
176 gactgggctt cagctctgtc tgaaaatctt tgcttcagag cacctcccta gtttgatctg 660
177 ataccctgcc tgacctgcc agagtccaga ggtcacggcg gccagccctt gcctccggga 720
178 aggttatctc aaatgctccc acagccctga cccttctgt tgctttgtcc cttgcagccc 780
179 aactcctctt tccgaccgcc gcagaaagac aaccccccaa gcctggtggc caaggccag 840
180 tccttgccct cggaccagcc ggtgggg acc ttc agc cct ctg acc act tcg gat 894
181 Thr Phe Ser Pro Leu Thr Thr Ser Asp
182 1 5
184 acc agc agc ccc cag aag tcc ctg cgc aca gcc ccg gcc aca ggc cag 942
185 Thr Ser Ser Pro Gln Lys Ser Leu Arg Thr Ala Pro Ala Thr Gly Gln
186 10 15 20 25

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```

188 ctt cca ggc cgg tct tcc cca gcg gga tcc ccc cgc acc tgg cac gcc      990
189 Leu Pro Gly Arg Ser Ser Pro Ala Gly Ser Pro Arg Thr Trp His Ala
190                               30                               35                               40
192 cag atc agc acc agc aac ctg tac ctg ccc cag gac ccc acg gtt gcc      1038
193 Gln Ile Ser Thr Ser Asn Leu Tyr Leu Pro Gln Asp Pro Thr Val Ala
194                               45                               50                               55
196 aag ggt gcc ctg gct ggt gag gac aca ggt gtt gtg aca cat gag cag      1086
197 Lys Gly Ala Leu Ala Gly Glu Asp Thr Gly Val Val Thr His Glu Gln
198                               60                               65                               70
200 ttc aag gct gcg ctc agg atg gtg gtg gac cag ggt gac ccc cgg ctg      1134
201 Phe Lys Ala Ala Leu Arg Met Val Val Asp Gln Gly Asp Pro Arg Leu
202                               75                               80                               85
204 ctg ctg gac agc tac gtg aag att ggc gag ggc tcc acc ggc atc gtc      1182
205 Leu Leu Asp Ser Tyr Val Lys Ile Gly Glu Gly Ser Thr Gly Ile Val
206 90                               95                               100                               105
208 tgc ttg gcc cgg gaa gaa cac tcg ggc cgc cag gtg gcc gtc aag atg      1230
209 Cys Leu Ala Arg Glu Glu His Ser Gly Arg Gln Val Ala Val Lys Met
210                               110                               115                               120
212 atg gac ctc aga aag cag cag cgc agg gag ctg ctc ttc aac gag      1275
213 Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu
214                               125                               130                               135
216 gtgggaggac aggttgggac acacacgggg gcgttgggga tgggcagtga gcagccagcc      1335
217 aggctggaca tctgtgagca ggggcagtgg gtggccatgc gtctgggcac tgtgcctggc      1395
218 actcaggccc ccacctgccc ccag gtg gtg atc atg cgg gac tac cag cac      1446
219                               Val Val Ile Met Arg Asp Tyr Gln His
220                               140                               145
222 ttc aac gtg gtg gag atg tac aag agc tac ctg gtg ggc gag gag ctg      1494
223 Phe Asn Val Val Glu Met Tyr Lys Ser Tyr Leu Val Gly Glu Glu Leu
224                               150                               155                               160
226 tgg gtg ctc atg gag ttc ctg cag gga gga gcc ctc aca gac atc gtc      1542
227 Trp Val Leu Met Glu Phe Leu Gln Gly Gly Ala Leu Thr Asp Ile Val
228                               165                               170                               175
230 tcc caa gtc ag gtgggcagct gggagggctg gaccctgagt gcaggctgcc      1593
231 Ser Gln Val Arg
232                               180
234 ctcaccatgg cctgcccagg gcaatgtggt cttctgcctg tggcccagaa gacttgggat      1653
235 gcctgggctc cctgcccctg tggggtaact gagaccaggg ggtcttggga gtggagaaga      1713
236 gaaggatagc ttctagccaa agctcaggcc ccagttttca ccagggtat ggcctgactg      1773
237 tgctgccaaa cagattgcct gggagctgtg gggcctagca ccagggactc ctactctgct      1833
238 cagccacccc acgacctgcc agagctaacg ttctctttca tcgggtggcc ccaccttcct      1893
239 gtccag g ctg aat gag gag cag att gcc act gtg tgt gag gct gtg ctg      1942
240 Leu Asn Glu Glu Gln Ile Ala Thr Val Cys Glu Ala Val Leu
241                               185                               190                               195
243 cag gcc ctg gcc tac ctg cat gct cag ggt gtc atc cac cgg gac atc      1990
244 Gln Ala Leu Ala Tyr Leu His Ala Gln Gly Val Ile His Arg Asp Ile
245                               200                               205                               210
247 aag agt gac tcc atc ctg ctg acc ctc gat ggc agg gtaggtccca      2036
248 Lys Ser Asp Ser Ile Leu Leu Thr Leu Asp Gly Arg
249                               215                               220

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251 tcctgtccct ggcacagcca cgctcccact tcctcctgat ccaccaactca ctcccttttc 2096
252 aaccgcag gtg aag ctc tcg gac ttc gga ttc tgt gct cag atc agc aaa 2146
253      Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Ile Ser Lys
254      225      230      235
256 gac gtc cct aag agg aag tcc ctg gtg gga acc ccc tac tgg atg gct 2194
257 Asp Val Pro Lys Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala
258      240      245      250
260 cct gaa gtg atc tcc agg tct ttg tat gcc act gag gtaaccgttc 2240
261 Pro Glu Val Ile Ser Arg Ser Leu Tyr Ala Thr Glu
262      255      260      265
264 cctccacccc ccagacctcc caaaagcaac ttggcaactg gcagctcttc tgctgtggcc 2300
265 cctccagtga gctcaccaaa agcagccctg gttttcagag tcccacctag tcaacaccct 2360
266 tccccctttc gatggggctg ctcttaccga gtgactttgc tgccaggaac gactcctgca 2420
267 agtgctttcc tcagctcaag ggcagaatgg ggtatggccg ggcctcctat gtatgatggc 2480
268 ctttctctga gtgactgaca gctgtgtccc tataggcagt ggtcactcat gcaggcagta 2540
269 actggccaca gggcagggtga ccaggggagg aaggagacag acccaccaag gagagctggg 2600
270 gccagctgtc cccctccac cactgctgcc accagaacgc agctaccaat gggccagggt 2660
271 ctggccatgg ggtcaggggac attttcctcc tgcag gtg gat atc tgg tct ctg 2713
272      Val Asp Ile Trp Ser Leu
273      270
275 ggg atc atg gtg att gag atg gta gat ggg gag cca ccg tac ttc agt 2761
276 Gly Ile Met Val Ile Glu Met Val Asp Gly Glu Pro Pro Tyr Phe Ser
277      275      280      285
279 gac tcc cca gtg caa gcc atg aag agg ctc cgg gac agc ccc cca ccc 2809
280 Asp Ser Pro Val Gln Ala Met Lys Arg Leu Arg Asp Ser Pro Pro Pro
281      290      295      300
283 aag ctg aaa aac tct cac aag gtc agttggcaca caagggtgcg acctcgcaga 2863
284 Lys Leu Lys Asn Ser His Lys Val
285      305      310
287 ccccatctct cctgaggcaa ggggaccaga acctgggctc ccagcatctc ccttccactg 2923
288 aagccacagg gtctgggctc ctggaaaagg ctctcttttc cccacacaaa acccgcacct 2983
289 ggggtgtggag cgcctcttac gcacaagttc gcatgtgcgc tccgacaagt cgctccccc 3043
290 ggctgtggca ggagagttgc tgcttggcag aagggttgct gcttggcagg cactggtcgg 3103
291 aagcccagtg gggcccatga gcagggaaag ccaggacacc agcaactccc tgctgtccag 3163
292 ggagggatcc ggagaagctt cactgagcac aaaccttca acccgtgtcg ggagatccat 3223
293 accatgattc gatgtccctg tccatcacgg cgagtggct catgtccat tcgttgca 3283
294 ccccgacaca gctaagccac agcgttcccc ttaaagccag tataagtga tggaaagtgg 3343
295 atacatgtaa ccttttttgc caaatcggcc ccaaccccgc aggccttact gtggacgccc 3403
296 cctgctggca ggtcagcacg gggtgataa gtggcaccgc catctggtgg ccaaaacaag 3463
297 aaatgtctca gagggctgaa gcctctctc taaaatagca aaaaaacaag agttctgtgg 3523
298 ccccaacaca aagctggatg ggaggaccaa caggaaacat cttccaagac aactggtcct 3583
299 tggagcccgc accgctaacc ccaaaattag catataaagc atgc 3627
302 <210> SEQ ID NO: 8
303 <211> LENGTH: 311
304 <212> TYPE: PRT
305 <213> ORGANISM: Homo sapiens
307 <400> SEQUENCE: 8
308 Thr Phe Ser Pro Leu Thr Thr Ser Asp Thr Ser Ser Pro Gln Lys Ser
309 1      5      10      15

```

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:660 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1021 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1047 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1060 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17